

Table S1. Primer sequences or TaqMan assay identifications and product sizes (bp) for real-time polymerase chain reaction

Gene	Sense / anti-sense sequence or TaqMan Assay Identification	bp
<i>Glut1</i>	CTG TCG GGT ATC AAT GCT GTG T	149
	CGT CCA GCT CGC TCT ACA AC	
<i>Vegfa</i>	AGC AGA TGT GAA TGC AGA CCA	112
	AGG ATT TAA ACC GGG ATT TCT TGC	
<i>Bmp-2</i>	Mm01962382_s1	101
<i>Bmp-4</i>	Mm03413826_mH	110
<i>Bmpr1a</i>	TGG GAG TGG ATC TGG ATT GC	120
	TCA CCA CGC CAT TTA CCC AT	
<i>Smad1</i>	GCT TCG TGA AGG GTT GGG G	147
	GCT TCG TGA AGG GTT GGG G	
<i>Smad5</i>	TTG TTC AGA GTA GGA ACT GCA AC	114
	GAA GCT GAG CAA ACT CCT GAT	
<i>Hey1</i>	CCG ACG AGA CCG AAT CAA TAA C	125
	TCA GGT GAT CCA CAG TCA TCT G	
<i>Runx2</i>	CTT CAC AAA TCC TCC CCA AGT G	150
	GGA ATG CGC CCT AAA TCA CTG	
<i>Sp7</i>	TTC TGC GGC AAG AGG TTC AC	125
	TTG CTC AAG TGG TCG CTT CT	
<i>Alpl</i>	GGG GTA CAA GGC TAG ATG GC	150
	CGG GCT CAA AGA GAC CTA AGA	
<i>Oc</i>	TTC TGC TCA CTC TGC TGA CC	99
	GCT TGG ACA TGA AGG CTT TGT	
<i>Eif2b1</i>	ACC TCC CTG GAA TAC TCT GAC T	136
	TCG CCC CGT CTT TGA TGA AT	
<i>Eif2b1</i>	Mm00460997_m1	83

Glut1: solute carrier family 2 (facilitated glucose transporter), member 1, *Vegfa*: vascular endothelial growth factor A, *Bmp-2*: bone morphogenetic protein 2, *Bmp-4*: bone morphogenetic protein 4, *Bmpr1a*: bone morphogenetic protein receptor, type 1A, *Smad1*: SMAD family member 1, *Smad5*: SMAD family member 5, *Hey1*: hairy/enhancer-of-split related with YRPW motif 1, *Runx2*: runt-related transcription factor 2, *Sp7*: osterix, *Alpl*: alkaline phosphatase, *Oc*: osteocalcin, *Eif2b1*: eukaryotic translation initiation factor 2B subunit 1 (alpha)

Table S2. Area under the curve (arbitrary unit) calculated to carry out the statistical analyses of the parameters evaluated over time (cell proliferation, cell migration and bone morphometry). The data are presented as mean \pm standard deviation and compared by Student's t test ($p \leq 0.05$)

Parameter	Control	Hypoxia	p-value
MSC proliferation	269.25 \pm 20.04	260.56 \pm 10.36	0.414
MSC migration	239.96 \pm 16.63	274.93 \pm 11.70	0.006
MC3T3-E1 proliferation	327.77 \pm 29.13	297.38 \pm 52.25	0.291
MC3T3-E1 migration	174.42 \pm 18.63	207.76 \pm 13.34	0.011
BV	3.85 \pm 1.81	4.07 \pm 1.31	0.748
BV/TV	30.05 \pm 14.01	31.97 \pm 10.55	0.720
BS	18.38 \pm 9.61	25.08 \pm 9.41	0.114
Tb.Th	0.22 \pm 0.05	0.23 \pm 0.05	0.780
Tb.N	0.49 \pm 0.22	0.57 \pm 0.25	0.395
BMD	0.27 \pm 0.14	0.34 \pm 0.09	0.160

MSC: mesenchymal stem cell, BV: bone volume, BV/TV: percentage of bone volume, BS: bone surface, Tb.Th: trabecular thickness, Tb.N: trabecular number, BMD: bone mineral density